

**RAW SEQUENCE LISTING**

RE-0001

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 09/518,763C

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IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/518,763C

DATE: 04/28/2008  
TIME: 10:34:27

Input Set : N:\AMC\US09518763C.raw  
Output Set: N:\CRF4\03192008\I518763C.raw

1 <110> APPLICANT: Blissard, Gary W.  
 2 Granados, Robert R.  
 3 Lin, Guangyun  
 4 <120> TITLE OF INVENTION: STABLE CELL LINES RESISTANT TO APOPTOSIS AND NUTRIENT  
 5 STRESS AND METHODS OF MAKING SAME  
 6 <130> FILE REFERENCE: BTI44  
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/518,763C  
 8 <141> CURRENT FILING DATE: 2000-03-03  
 9 <160> NUMBER OF SEQ ID NOS: 11  
 10 <170> SOFTWARE: PatentIn Ver. 3.1  
 12 <210> SEQ ID NO: 1  
 13 <211> LENGTH: 900  
 14 <212> TYPE: DNA  
 15 <213> ORGANISM: Autographa californica nucleopolyhedrovirus  
 16 <220> FEATURE:  
 17 <221> NAME/KEY: CDS  
 18 <222> LOCATION: (1)..(897)  
 19 <300> PUBLICATION INFORMATION:  
 20 <301> AUTHORS: Ayres, Martin D.  
 21 Howard, Stephen C.  
 22 Kuzio, John  
 23 Lopez-Ferber, Miguel  
 24 Possee, Robert D.  
 25 <302> TITLE: The Complete DNA Sequence of Autographa californica  
 26 Nuclear Polyhedrosis Virus  
 27 <303> JOURNAL: Virology  
 28 <304> VOLUME: 202  
 29 <305> ISSUE: 2  
 30 <306> PAGES: 586-605  
 31 <307> DATE: 1994  
 32 <308> DATABASE ACCESSION NO: L22858  
 33 <309> DATABASE ENTRY DATE: 1999-03-08  
 34 <313> RELEVANT RESIDUES: 116492 TO 117391  
 35 <400> SEQUENCE: 1  
 36 atg tgt gta att ttt ccg gta gaa atc gac gtg tcc cag acg att att 48  
 37 Met Cys Val Ile Phe Pro Val Glu Ile Asp Val Ser Gln Thr Ile Ile  
 38 1 5 10 15  
 39 cga gat tgt cag gtg gac aaa caa acc acc aga gag ttg gtg tac att aac 96  
 40 Arg Asp Cys Gln Val Asp Lys Gln Thr Arg Glu Leu Val Tyr Ile Asn  
 41 20 25 30  
 42 aag att atg aac acg caa ttg aca aaa ccc gtt ctc atg atg ttt aac 144  
 43 Lys Ile Met Asn Thr Gln Leu Thr Lys Pro Val Leu Met Met Phe Asn  
 44 35 40 45

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45	att tcg ggt cct ata cga agc gtt acg cgc aag aac aac aat ttg cgc	192
46	Ile Ser Gly Pro Ile Arg Ser Val Thr Arg Lys Asn Asn Asn Leu Arg	
47	50 55 60	
48	gac aga ata aaa tca aaa gtc gat gaa caa ttt gat caa cta gaa cgc	240
49	Asp Arg Ile Lys Ser Lys Val Asp Glu Gln Phe Asp Gln Leu Glu Arg	
50	65 70 75 80	
51	gat tac agc gat caa atg gat gga ttc cac gat agc atc aag tat ttt	288
52	Asp Tyr Ser Asp Gln Met Asp Gly Phe His Asp Ser Ile Lys Tyr Phe	
53	85 90 95	
54	aaa gat gaa cac tat tcg gta agt tgc caa aat ggc agc gtg ttg aaa	336
55	Lys Asp Glu His Tyr Ser Val Ser Cys Gln Asn Gly Ser Val Leu Lys	
56	100 105 110	
57	agc aag ttt gct aaa att tta aag agt cat gat tat acc gat aaa aag	384
58	Ser Lys Phe Ala Lys Ile Leu Lys Ser His Asp Tyr Thr Asp Lys Lys	
59	115 120 125	
60	tct att gaa gct tac gag aaa tac tgt ttg ccc aaa ttg gtc gac gaa	432
61	Ser Ile Glu Ala Tyr Glu Lys Tyr Cys Leu Pro Lys Leu Val Asp Glu	
62	130 135 140	
63	cgc aac gac tac tac gtg gcg gta tgc gtg ttg aag ccg gga ttt gag	480
64	Arg Asn Asp Tyr Tyr Val Ala Val Cys Val Leu Lys Pro Gly Phe Glu	
65	145 150 155 160	
66	aac ggc agc aac caa gtg cta tct ttc gag tac aac ccg att ggt aac	528
67	Asn Gly Ser Asn Gln Val Leu Ser Phe Glu Tyr Asn Pro Ile Gly Asn	
68	165 170 175	
69	aaa gtt att gtg ccg ttt gct cac gaa att aac gac acg gga ctt tac	576
70	Lys Val Ile Val Pro Phe Ala His Glu Ile Asn Asp Thr Gly Leu Tyr	
71	180 185 190	
72	gag tac gac gtc gta gct tac gtg gac agt gtg cag ttt gat ggc gaa	624
73	Glu Tyr Asp Val Val Ala Tyr Val Asp Ser Val Gln Phe Asp Gly Glu	
74	195 200 205	
75	caa ttt gaa gag ttt gtg cag agt tta ata ttg ccg tcg tcg ttc aaa	672
76	Gln Phe Glu Glu Phe Val Gln Ser Leu Ile Leu Pro Ser Ser Phe Lys	
77	210 215 220	
78	aat tcg gaa aag gtt tta tat tac aac gaa gcg tcg aaa aac aaa agc	720
79	Asn Ser Glu Lys Val Leu Tyr Tyr Asn Glu Ala Ser Lys Asn Lys Ser	
80	225 230 235 240	
81	atg atc tac aag gct tta gag ttt act aca gaa tcg agc tgg ggc aaa	768
82	Met Ile Tyr Lys Ala Leu Glu Phe Thr Thr Glu Ser Ser Trp Gly Lys	
83	245 250 255	
84	tcc gaa aag tat aat tgg aaa att ttt tgt aac ggt ttt att tat gat	816
85	Ser Glu Lys Tyr Asn Trp Lys Ile Phe Cys Asn Gly Phe Ile Tyr Asp	
86	260 265 270	
87	aaa aaa tca aaa gtg ttg tat gtt aaa ttg cac aat gta act agt gca	864
88	Lys Lys Ser Lys Val Leu Tyr Val Lys Leu His Asn Val Thr Ser Ala	
89	275 280 285	
90	ctc aac aaa aat gta ata tta aac aca att aaa taa	900
91	Leu Asn Lys Asn Val Ile Leu Asn Thr Ile Lys	
92	290 295	

94 <210> SEQ ID NO: 2

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95 <211> LENGTH: 299  
96 <212> TYPE: PRT  
97 <213> ORGANISM: *Autographa californica* nucleopolyhedrovirus  
98 <400> SEQUENCE: 2  
99 Met Cys Val Ile Phe Pro Val Glu Ile Asp Val Ser Gln Thr Ile Ile  
100 1 5 10 15  
101 Arg Asp Cys Gln Val Asp Lys Gln Thr Arg Glu Leu Val Tyr Ile Asn  
102 20 25 30  
103 Lys Ile Met Asn Thr Gln Leu Thr Lys Pro Val Leu Met Met Phe Asn  
104 35 40 45  
105 Ile Ser Gly Pro Ile Arg Ser Val Thr Arg Lys Asn Asn Asn Leu Arg  
106 50 55 60  
107 Asp Arg Ile Lys Ser Lys Val Asp Glu Gln Phe Asp Gln Leu Glu Arg  
108 65 70 75 80  
109 Asp Tyr Ser Asp Gln Met Asp Gly Phe His Asp Ser Ile Lys Tyr Phe  
110 85 90 95  
111 Lys Asp Glu His Tyr Ser Val Ser Cys Gln Asn Gly Ser Val Leu Lys  
112 100 105 110  
113 Ser Lys Phe Ala Lys Ile Leu Lys Ser His Asp Tyr Thr Asp Lys Lys  
114 115 120 125  
115 Ser Ile Glu Ala Tyr Glu Lys Tyr Cys Leu Pro Lys Leu Val Asp Glu  
116 130 135 140  
117 Arg Asn Asp Tyr Tyr Val Ala Val Cys Val Leu Lys Pro Gly Phe Glu  
118 145 150 155 160  
119 Asn Gly Ser Asn Gln Val Leu Ser Phe Glu Tyr Asn Pro Ile Gly Asn  
120 165 170 175  
121 Lys Val Ile Val Pro Phe Ala His Glu Ile Asn Asp Thr Gly Leu Tyr  
122 180 185 190  
123 Glu Tyr Asp Val Val Ala Tyr Val Asp Ser Val Gln Phe Asp Gly Glu  
124 195 200 205  
125 Gln Phe Glu Glu Phe Val Gln Ser Leu Ile Leu Pro Ser Ser Phe Lys  
126 210 215 220  
127 Asn Ser Glu Lys Val Leu Tyr Tyr Asn Glu Ala Ser Lys Asn Lys Ser  
128 225 230 235 240  
129 Met Ile Tyr Lys Ala Leu Glu Phe Thr Thr Glu Ser Ser Trp Gly Lys  
130 245 250 255  
131 Ser Glu Lys Tyr Asn Trp Lys Ile Phe Cys Asn Gly Phe Ile Tyr Asp  
132 260 265 270  
133 Lys Lys Ser Lys Val Leu Tyr Val Lys Leu His Asn Val Thr Ser Ala  
134 275 280 285  
135 Leu Asn Lys Asn Val Ile Leu Asn Thr Ile Lys  
136 290 295  
138 <210> SEQ ID NO: 3  
139 <211> LENGTH: 38  
140 <212> TYPE: DNA  
141 <213> ORGANISM: Artificial Sequence  
142 <220> FEATURE:  
143 <223> OTHER INFORMATION: Description of Artificial Sequence:  
144 oligonucleotide primer

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145 <400> SEQUENCE: 3  
146 ctagaaggtaa gaaagatgcc agcggctggg cgtaatag 38  
148 <210> SEQ ID NO: 4  
149 <211> LENGTH: 38  
150 <212> TYPE: DNA  
151 <213> ORGANISM: Artificial Sequence  
152 <220> FEATURE:  
153 <223> OTHER INFORMATION: Description of Artificial Sequence:  
154 oligonucleotide primer  
155 <400> SEQUENCE: 4  
156 ctagctatta cgaccagccg ctggcatctt tccaaactt 38  
158 <210> SEQ ID NO: 5  
159 <211> LENGTH: 30  
160 <212> TYPE: DNA  
161 <213> ORGANISM: Artificial Sequence  
162 <220> FEATURE:  
163 <223> OTHER INFORMATION: Description of Artificial Sequence: p35upEcoRI  
164 primer  
165 <400> SEQUENCE: 5  
166 cagaattcat gtgtgttaatt tttccggtag 30  
168 <210> SEQ ID NO: 6  
169 <211> LENGTH: 33  
170 <212> TYPE: DNA  
171 <213> ORGANISM: Artificial Sequence  
172 <220> FEATURE:  
173 <223> OTHER INFORMATION: Description of Artificial Sequence: p35lowXbaI-NO  
174 stop primer  
175 <400> SEQUENCE: 6  
176 ttttgctcta gatttaattt tgtttaatat tac 33  
178 <210> SEQ ID NO: 7  
179 <211> LENGTH: 35  
180 <212> TYPE: DNA  
181 <213> ORGANISM: Artificial Sequence  
182 <220> FEATURE:  
183 <223> OTHER INFORMATION: Description of Artificial Sequence:  
184 p35lowXbaI-Stop primer  
185 <400> SEQUENCE: 7  
186 aatgctctag attatttaat tgtgttaat attac 35  
188 <210> SEQ ID NO: 8  
189 <211> LENGTH: 15  
190 <212> TYPE: DNA  
191 <213> ORGANISM: Artificial Sequence  
192 <220> FEATURE:  
193 <223> OTHER INFORMATION: Description of Artificial Sequence:  
194 p166-p35 linker DNA  
195 <400> SEQUENCE: 8  
196 ttaaacacaaa ttaaaa 15  
198 <210> SEQ ID NO: 9  
199 <211> LENGTH: 5

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Input Set : N:\AMC\US09518763C.raw  
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200 <212> TYPE: PRT  
201 <213> ORGANISM: Artificial Sequence  
202 <220> FEATURE:  
203 <223> OTHER INFORMATION: Description of Artificial Sequence:  
204 p166-p35 linker polypeptide  
205 <400> SEQUENCE: 9  
206 Leu Asn Thr Ile Lys  
207 1 5  
209 <210> SEQ ID NO: 10  
210 <211> LENGTH: 54  
211 <212> TYPE: DNA  
212 <213> ORGANISM: Artificial Sequence  
213 <220> FEATURE:  
214 <223> OTHER INFORMATION: Description of Artificial Sequence:  
215 p166-p35-AcV5 linker DNA  
216 <400> SEQUENCE: 10  
217 ttaaacacaa ttaaatctag aagttggaaa gatgccagcg gctggtcgta atag 54  
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220 <211> LENGTH: 16  
221 <212> TYPE: PRT  
222 <213> ORGANISM: Artificial Sequence  
223 <220> FEATURE:  
224 <223> OTHER INFORMATION: Description of Artificial Sequence:  
225 p166-p35-AcV5 linker polypeptide  
226 <400> SEQUENCE: 11  
227 Leu Asn Thr Ile Lys Ser Arg Ser Trp Lys Asp Ala Ser Gly Trp Ser  
228 1 5 10 15

**VERIFICATION SUMMARY**

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L:7 M:270 C: Current Application Number differs, Wrong Format